

Residues 1-172 fused to 990-1178 from SEQ ID NO:29, reverse-translated and aligned with Cao 2005/0084850 SEQ ID NO:5

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<!--StartFragment-->RESULT 5
US-10-347-669-5
; Sequence 5, Application US/10347669
; Publication No. US20050084850A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/10/347,669
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1610
; TYPE: DNA
; ORGANISM: human
US-10-347-669-5

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Alignment Scores:

Pred. No.:	2.73e-59	Length:	1610
Score:	1833.80	Matches:	360
Percent Similarity:	96.5%	Conservative:	0
Best Local Similarity:	96.5%	Mismatches:	1
Query Match:	99.1%	Indels:	12
DB:	11	Gaps:	1

US-09-830-972A-29FUSA (1-361) x US-10-347-669-5 (1-1610)

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Qy      1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20
      |||
Db      132 ATGGAAGACCTGGACCACTCTCCTCTGGTCTCGTCTCGGACAGCCACCCCGGCGCGAG 191

Qy      21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGlu 40
      |||
Db      192 CCCCGTTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAAGAGGAGGAG 251

Qy      41 GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla 60
      |||
Db      252 GAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAAGGAAGCCCGCC 311

Qy      61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
      |||
Db      312 GCCGGGCTGTCCCGGCCCCAGTGCCACCCGCCCTGCGCGCGGCGGCCCTGATGGAC 371

Qy      81 PheGlyAsnAspPheValProProAlaProArgGlyProLeuProAlaAlaProProVal 100
      |||
Db      372 TTGGAAATGACTTCTGTGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 431

Qy      101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
      |||
Db      432 GCCCGGAGCGGCGAGCCGTCTTGGGACCCGAGCCCGGTGCTGTCGACCGTGCCCGCGCCA 491

Qy      121 SerProLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspGluProPro 140
      |||
Db      492 TCCCGCTGTCTGTGTCGCCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAGCCTCG 551

Qy      141 AlaArgProProProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
      |||
Db      552 GCCCGCCTCCCTCTCTCCCGGCCAGCGTGAGCCCGCAGGCAGGCCGTGTGGACC 611

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Qy      161  ProProAlaProAlaProAlaAlaProProSerThrSer----- 173
      |||
Db      612  CCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCGCCCAAGCGCAGGGGC 671
      |||
Qy      174  -----ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 188
      |||
Db      672  TCCTCGGGCTCAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAGAAGACTGGAGTG 731
      |||
Qy      189  ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal 208
      |||
Db      732  GTGTTTGGTGCACGCTATTCTCTGCTGCTTCATTGACAGTATTGACGATTGTGAGCGTA 791
      |||
Qy      209  ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly 228
      |||
Db      792  ACAGCCTACATTGCCTTGCCCTGCTCTCTGTGACCATCAGCTTAGGATATACAAGGGT 851
      |||
Qy      229  ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer 248
      |||
Db      852  GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGCATATCTGGAATCT 911
      |||
Qy      249  GluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal 268
      |||
Db      912  GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTC 971
      |||
Qy      269  AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 288
      |||
Db      972  AACTGCACGATAAAGGAATCAGGCGCCTCTTCTAGTTGATGATTTAGTTGATTCTCTG 1031
      |||
Qy      289  LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr 308
      |||
Db      1032  AAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCTTGTTTAATGGTCTGACA 1091
      |||
Qy      309  LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln 328
      |||
Db      1092  CTACTGATTTGGCTCTCATTCTCACTCTTCAGTGTTCTGTTATTATGAACGCATCAG 1151
      |||
Qy      329  AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys 348
      |||
Db      1152  GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA 1211
      |||
Qy      349  IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 361
      |||
Db      1212  ATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA 1250
<!--EndFragment-->

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